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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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seq length: 2000000000
                              A_Geneseq_101002:*

1: /SIDS2/gcgdata/g
2: /SIDS2/gcgdata/g
4: /SIDS2/gcgdata/g
4: /SIDS2/gcgdata/g
5: /SIDS2/gcgdata/g
6: /SIDS2/gcgdata/g
6: /SIDS2/gcgdata/g
7: /SIDS2/gcgdata/g
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87
1 ALYKKFKKKLLKSL
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J: //SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT: *
1: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1988.DAT: *
2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
3: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
3: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
4: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
5: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
6: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
7: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
9: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
9: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
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0: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: *
2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: *
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Copyright (c) 1993 - 2002 Compu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \(\SIDS2\)gcgdata\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\) = \mblue \text{IDAI}\); \(\SIDS2\)gcgdata\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\) = \mblue \text{IDAI}\); \(\SIDS2\)gcgdata\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\) = \mblue \text{IDAI}\); \(\sin \text{SIDS2}\)gcgdata\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\) = \mblue \text{IDAI}\); \(\sin \text{SIDS2}\)gcgdata\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\)emblu\(\gamma\)AA1988\(\gamma\)DAI\(\pi\); \(\sin \text{SIDS2}\)gcgdata\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\)geneseq\(\gamma\)emblu\(\gamma\)a\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamma\)i\(\gamm
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26.357 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10	9	- 00	7	6	5	4	w	2	1	Result No.
77	81	82	83	87	87	87	87	87	87	Score
88.5	93.1	94.3	95.4	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
18	18	18	18	35	25	20	19	19	18	Length DB
20	20	20	20	20	20	20	20	20	20	DB
AAY57505	AAY57503	AAY57500	AAY57504	AAY57497	AAY57496	AAY57502	AAY57501	AAY57499	AAY57465	ID
Antimicrobial pept	_	,							Antimicrobial pept	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	<u>н</u> . О	14	13	12	11
45	45		45	46	46	46	46	46	46	46	47	47	47	48	48	48	50	52	52	52	53	56	57	61	62	62	62	62	64	66	66	66	66	66
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780	77	78	74	-	02	28	28	<u>_</u>	سر ندا	4	139	574	74	28	13	213	7	23	AAR58975	75	74	39	4	AAR13925	AAR13936	AAR13930	AAR13928	AAR13926	AAY57472	AAY68002	AAW10352	AAY68001	AAW10351	AAR13927
imicrobial	<u>.</u> .	crobial oli	imicrobial pep	ngiogenic p	7	: pept		amph	e of	nce of amphi	eric alph	imicrobial pep	ୁ.	\vdash	_		\cap	_	Fragment of platel	Antimicrobial pept	2	Ω	rol	ic	j. 0,	ic oligopep	ic oligopep	c oligopep	nicrobial pep	Antibacterial pept	-	Antibacterial pept	ntibacterial pe	Cationic oligopept

ALIGNMENTS

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AAY57465
IID AAY5
XX
AC AAY5
AC AAY5
XX 25-F
XX Anti
PT Aga.
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
         Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi \,\cdot\,
                                                WPI; 1999-527417/44.
                                                                           Yeaman MR,
                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                             18-FEB-1998;
                                                                                                                                                      17-FEB-1999;
                                                                                                                                                                                26-AUG-1999
                                                                                                                                                                                                      W09942119-A1
                                                                                                                                                                                                                                Oryctolagus cuniculus.
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                          Antimicrobial peptide RP-1 SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                     25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                              AAY57465;
                                                                                                                                                                                                                                                                                                                                                                                     AAY57465 standard; Peptide; 18
                                                                         Shen AJ;
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                             98US-0025319.
                                                                                                                                                     99WO-US03350
                                                                                                                                                                                                                                                                                                                                                                                        AA.
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RESULT 2
AAY57499
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBEZBXBKB and its derivatives selected from XZBEZBXBKB, BXZXB, BXZXES, XBBXZBBX and BREXZBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXXXXB, XBBZXXBB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an antimicrobial peptide (AP) for directivity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 106; 166pp; English
The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZEBENBANB and its derivatives selected from XZBBZBNBAB, BXZXB, BXZXZB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXXBBX, BXXBXXBB, XBBZXXBB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences used in the exemplification of the present invention
                                                                                                                                                                                                     Antimicrobial peptides for potentiating against bacteria and fungi \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57499 standard; Peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                            WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                               Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000 (first entry)
                                                                                                                                                                   Disclosure; Page 58; 166pp; English
                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST
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                                                                                                                                                                                                                                                                                                                                                                       98US-0025319
                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US03350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungal; bacterial;
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Pred. No.
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8e-06;
                                                                                                                                                                                                                            antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutrophil; apoptosis
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RESULT 3
AAY57501
ID AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                             XBBZXXBBXXBBX; where B = at least one positively charged amino acid; x = at least one non-polar hydrophobic amino acid; z = at least one aromatic amino acid, and where B, x and z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
                                                                                                                                                                                                                          activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting of a first peptide template XZBZBXBXB and its derivatives essentially of a first peptide template XZBZBXBXB and its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY57501;
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                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial
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                                                                                                                                                                                                           selected from XZBBZBXBXB,
                                                                                                                                                                                                                                                                                                     The present
                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 59; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527417/44
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                                 sequences
                                                                                                                                                                        selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in the exemplification of the present invention
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                                 used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection;
                                                                                                                                                                                                                                                                                                     invention describes an antimicrobial peptide (AP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide 19C-RP-1
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Pred. No. 8.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:39
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                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                      The present invention describes an antimicrobial peptide (AP) for dire activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, BXZXXB, XBBXXXBBX and BBXZBBXZ; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000 (first entry)
                                                                                                                                                          the group consisting of XBBXXBBX, XBBXXBBX, BXXBXXBB, and XBBZXXBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57577 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi \,\cdot\,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1998;
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                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                        (b) a second peptide template XBBXX and their derivatives selected from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 18; Conserv
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                                                                             Local Similarity
 N
                              ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection;
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                                                                                                                             20 AA;
                                                               Conservative
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                                                                             100.0%; Score 87; DB 20; 100.0%; Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 8.4e-06;
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AAY57496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the group consisting of XBBXBBX, XBBXXBBX, XBBXXXBB, XBBXXBB, XBBXXXBB, XBBXXXBB, XBBXXXBB, XBAXXBB, XBAXXBB, XBAXBX, XBAXBX, XBAXXBB, XBAXXBB, XBAXXBB, XBAXXBB, XBAXXBB, XBAXXBB, XBAXXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBBXB and its derivatives selected from XZBBZBXBXB, BXZXZB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibiotic; infection; fungal; bacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 126; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                         Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35
                                                                                                                                                                                                      AAY57497 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences used in the exemplification of the present invention
                                                                                    25-FEB-2000
                                                                                                                                                AAY57497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      1 ALYKKFKKKLLKSLKRLG
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                                                                                    (first entry)
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                                26-AUG-1999
                                                                                                                                                                                Oryctolagus cuniculus
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY57504 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 126; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              peptide RP-1-10F SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0025319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US03350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87; DB 20;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AAY57500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
           WPI; 1999-527417/44
                                           Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXBX, XBBZXXBB, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.
                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                           18-FEB-1998;
                                                                                                                                                                                                       W09942119-A1
                                                                                                                                         17-FEB-1999;
                                                                                                                                                                                                                                     Oryctolagus cuniculus
                                                                                                                                                                                                                                                                              antibiotic; infection; fungal; bacterial; neutrophil; apoptosis
                                                                                                                                                                                                                                                                                            Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                          26-AUG-1999
                                                                                                                                                                                                                                                                                                                                  Antimicrobial
                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  AAY57500;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57500 standard; Peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXB, BXZXZB, XBBXZXBBX and BBXZBBXZ; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 59; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKKFKKKFLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                 peptide 13C-RP-1 SEQ ID NO:38.
                                                                                                       98US-0025319.
                                                                                                                                         99WO-US03350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0025319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.4%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 83; DB 20;
Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
            The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting
                                                                                          Disclosure;
                                                                                                                   against bacteria and fungi
                                                                                                                               Antimicrobial peptides for
                                                                                                                                                               WPI; 1999-527417/44.
                                                                                                                                                                                        Yeaman MR, Shen AJ
                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                                                                                                 18-FEB-1998;
                                                                                                                                                                                                                                                                            17-FEB-1999;
                                                                                                                                                                                                                                                                                                         26-AUG-1999
                                                                                                                                                                                                                                                                                                                                     W09942119-A1
                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                          antibiotic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY57503,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY57503 standard; Peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXZB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organisms such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 58; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial peptides for potentiating antimicrobial agents active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALYKKFKKKLLKCLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                     Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention describes an antimicrobial peptide (AP) for direct
for potentiating antimicrobial agents active against
uch as bacteria and fungi. The AP comprises: (a) a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                 98US-0025319
                                                                                                                                                                                                                                                                            99WO-US03350
first peptide template XZBZBXBXB and its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.38;
                                                                                                                                                                                                                                                                                                                                                                                                         fungal; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                            potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                    neutrophil; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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RESULT 10
AAY57505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                    The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXLB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from
more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
                                                                          the group consisting of XBBXXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or
                                                                                                                                                                                                                                                                                                                   Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                      Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXB, XBBZXXBB, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY57505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57505 standard; Peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selected from X2BBZBXBXB, BXZXB, BXZXZXB, XBBX2XBBX and BBXZBBXZ; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; fungal; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0025319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US03350
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94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
5.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neutrophil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 11
AAR13927
                                            RESULT 12
AAW10351
                                                                                                                                                          Db
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                                                                                                   QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                       Matches
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                          This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alpha-helical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7.
                                                                                                                                                                                                                                                           Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9112815-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cationic oligopeptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR13927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR13927 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         human platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                                                                                                                                                                                                   aeruginosa etc.
                                                                                                                                                                                                                                                                                                 WPI; 1991-281214/38.
                                                                                                                                                                                                                                                                                                                    Darveau RP,
                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                       19-FEB-1991;
23-FEB-1990;
                  AAW10351;
                                    AAW10351 standard;
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                 Claim 17; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1991;
22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ARYKKFKKKFLKSLKRLG 18
                                                                                  1 ALYKKLLKKLLKSAKKLG 18
                                                                                                     1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AA;
                                                                                                                                                           18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                    Blake JJ,
(first entry)
                                                                                                                                                                                                                                                                                                                                                       91US-0655321.
90US-0484020.
                                                                                                                                                                                                                                                                                                                                                                                  91WO-US01224
                                    peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.5%;
                                                                                                                                75.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                   Cosand WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 77; DB 20;
Pred. No. 0.00021;
                                                                                                                                Score 66; DB 12; Pred. No. 0.0076;
                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                       Mismatches
                                                                                                                                          DB 12;
                                                                                                                       ω
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                                                                                                                                        Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                         0;
                                                                                                                                  RESULT 13
AAY68001
                                                                                                                                                                                                                                               dd
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firca JR, I
Stafford D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-077224/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9640251-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OPHI-) OPHIDIAN PHARM INC
   US5998381-A
                                                                                                                                                                                                                                              Sequence
                     Synthetic
                                                                                     11-APR-2000
                                                                                                        AAY68001;
                                                                                                                                                                       1 ALYKKLLKKLLKSAKKLG
                                                                                                                                                                                         1 ALYKKFKKKLLKSLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Panasik N,
                                                                                                                                                                                                                                               18 AA;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams JA;
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0482191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US10227
                                                                                                                                                                                                                    75.9%;
                                                                                                                                                                        18
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13

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The present sequence is an antibacterial peptide C18G, which was CC modified by adding a Cys-amide to the carboxy terminus. This was used to CC produce an immunoadapter conjugate. Making a conjugate comprises CC covalently linking a surface-binding ligand (SBL) to a hapten via a ccompound with immunoglobulin (Ig) under conditions that allow for non-CC compound with immunoglobulin (Ig) under conditions that allow for non-CC covalent binding of the Ig to the hapten of the compound. The conjugate CC can be used for the diagnosis, prevention and treatment of microbial CC infections, e.g. sepsis, influenza, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can CC conjugate can use small molecule targeting ligands to efficiently CC direct otherwise unreactive Ig to microbial targets. This targeting can Ig conjugate can use small molecule targeting ligands to efficiently CC allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial compsns. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; endocrinology; antibodiotic; antibody; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 39; Page 150; 227pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial peptide C18G for immunoadapter synthesis
                                                                                                                            Antibacterial peptide C18G SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                      AAY68001 standard; peptide; 18
bacterial infection; antibacterial; fimbriae-binding compound; sepsis
                                   Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pugh C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 18;
Pred. No. 0.0076;
                                                                                                                                                                                                                                                                                                                                                                                                    AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schatz RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shekhani MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC group which provides a site for chemical modification remote from the CC mannose and a pharmaceutically carrier; and (b) administering the CC fimbriae-binding compounds to the subject. Administration of one or more CC fimbriae-binding compounds can be used for treating subjects with CC symptoms of and for subjects at risk from bacterial diseases. Treatment CC of and prevention of blood-borne and toxin mediated diseases. Treatment CC particular sepsis in humans and other animals can be carried out and the CC in vivo neutralisation of the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their CC cell binding specificity's through conjugation to reporter substances CC such as dyes, luminescent or fluorescent molecules and enzymes. The CC compounds also inhibit the agglutination of yeast cells induced by type CC 1 pili bearing bacteria. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
W09640251-A1
                                                  Modified-site
                                                                                                    Synthetic
                                                                                                                                                        hapten;
                                                                                                                                                               Antimicrobial; immunoglobulin; surface binding ligand;
                                                                                                                                                                                                    Antibacterial peptide C19G for immunoadapter synthesis
                                                                                                                                                                                                                                             22-SEP-1997
                                                                                                                                                                                                                                                                                 AAW10352;
                                                                                                                                                                                                                                                                                                           AAW10352 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         configuration, an alpha-aromatic or heteroaromatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described is a method of treatment for bacterial disease comprising:

(a) providing a subject with symptoms of bacterial disease with one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              more fimbriae-binding compounds comprising a mannose of an anomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 39; Column 84; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N^{-}(phenylalanyl)^{-4}-aminophenyl-alpha-D-mannopyranoside \ or \ its \ cysteinyl \ derivative \ useful for \ diagnosing \ and \ treating \ bacterial \ diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-115173/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shekhani MS, Anderson B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Therapeutic formulation comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                      1 ALYKKLLKKLLKSAKKLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                    sepsis; influenza; viremia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                  antibodiotic; antibody; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0760903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0760903
                           /note= "In amide form"
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firca JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 21;
Pred. No. 0.0076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                      fungemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                  neurology; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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AAY68002
ID AAY6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                       Shekhani MS,
                                                                             (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                      06-DEC-1996;
                                                                                                                                                                                         06-DEC-1996;
                                                                                                                                                                                                                                                    07-DEC-1999
                                                                                                                                                                                                                                                                                                             US5998381-A
                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                             Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial peptide C19G SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally leads to the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the compound with immunoglobulin (Ig) under conditions that allow for non-covalent binding of the Ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. sepsis, influenza, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY68002 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accessible to Ig, or are incapable of stimulating antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a peptide designated C19G. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently linking a surface-binding ligand (SBL) to a hapten via a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Firca JR, I
Stafford D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial compsns. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated with immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-077224/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKLLKKLLKSAKKLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panasik N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams JA;
                    Anderson B,
                                                                                                                                   96US-0760903
                                                                                                                                                                                            96US-0760903
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                 Firca JR;
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Pred. No.
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Example 39; Column 84; 89pp; English.
                                                                                                                                                                    Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and treating bacterial diseases -
                                                                                                                                                                                              WPI; 2000-115173/10.
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The present invention describes a therapeutic formulation comprising CC N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also CC described is a method of treatment for bacterial disease comprising: CC (a) providing a subject with symptoms of bacterial disease with one or CC (a) providing a subject with symptoms of bacterial disease with one or CC more fimbriae-binding compounds comprising a mannose of an anometic CC mannose by a glycosidic or pseudoglycosidic linkage and a functional CC group which provides a site for chemical modification remote from the CC fimbriae-binding compound to the subject. Administration of one or more Cf fimbriae-binding compound to the subject. Administration of one or more CC fimbriae-binding compounds can be used for treating subjects with CC symptoms of and for subjects at risk from bacterial diseases. Treatment CC fand prevention of blood-borne and toxin mediated diseases in CC particular sepsis in humans and other animals can be carried out and the CC in vivo neutralisation of the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their CC cell binding specificity's through conjugation to reporter substances CC such as dyes, luminescent or fluorescent molecules and enzymes. The CC compounds also inhibit the agglutination of yeast cells induced by type CC avennification of the present sequence is used in the exemplification of the present invention.

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Query Match
Matches
         Best
                                     Sequence
        Local Similarity
                                      19 AA;
 Conservative
          75.98;
77.88;
         Score 66; DB 21,
Pred. No. 0.008;
 Mismatches
                   DB 21; Length 19;
  3; Indels
   0;
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B QΥ 1 ALYKKLLKKLLKSAKKLG 18 1 ALYKKFKKKLLKSLKRLG 18

Search completed: December 24, 2002, 09:18:27 Job time : 92 secs

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Database
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    Query
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1: pir1:*
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Gapop 10.0 ,
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A70358
H75179
$70634
B90095
T49679
$69133
H71033
                                                                                              S56250
T39376
S59050
T27670
B64316
                                                                                                                                                                                              B90286
T41735
T17679
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$38002
JC5923
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E86212
F35270
F90087
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31.462 Million cell updates/sec
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Result

No.

Query Match

55.2%;

Score 48;

DB 2;

Length 540;

						prem 1
	ALIGNMENTS					
heat shock protein	AF2111		248	47.1	41	45
membrane-bound lyt	F84960	2	221	47.1	41	44
hypothetical prote	T01194		211	47.1	41	43
hepatoma-derived q	JC7163		203	47.1	41	42
myoqlobin, body wa	A55139		153	47.1	41	41
hypothetical prote	в90523		143	47.1	41	40
hypothetical prote	T27846		118	47.1	41	39
hypothetical prote	T27847		109	47.1	41	38
platelet factor 4	A26774		105	47.1	41	37
platelet factor 4	PFHU4		10:	47.1	41	36
hypothetical prote	G81882		76	47.1	41	ω
valine-tRNA ligase	A70423		1165	48.3	42	34
1,4-alpha-glucan b			70,	48.3	42	. W
hypothetical prote	T42646		559	48.3	42	3.2
probable transport			558	48.3	4.2) (J.
aldehyde dehydroge			488	48.3	42	30

A;Reference number: A70300; MUID:98196666; PMID:9537320 A:Reference number: A70358 C;Species: Methanococcus jannaschii C;Sate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: C64470 C;Accession: C64470 C;Accession: C64470 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, J.M.; Glodek, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Sclence 273, 1058-1073, 1996 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Accession: C64470 A;Accession: C64470 A;Molecule type: DNA A;Residues: 1-540 <AQF> A;Cross-references: GB:AE000700; NID:92983248; PIDN:AAC06848.1; PID:92983253; C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999 C;Accession: A70358 A:Experimental source: strain VF5 C;Genetics: C;Accession: A70358 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; δÃ A;Gene: A;Status; preliminary; nucleic acid sequence not shown; translation not shown topoisomerase I - Aquifex aeolicus DЬ A; Start codon: TTG A; Map position: FOR1313161-1314624 C; Genetics A;Cross-references: GB:U67576; GB:L77117; NID:g2826398; PIDN:AAB99372.1; PID:g1592008 A; Molecule type: DNA A; Residues: 1-487 <BUL> A:Status: preliminary; nucleic acid sequence not shown; translation not shown hypothetical protein MJ1364 - Methanococcus jannaschii Matches Query Match Best Local Similarity 264 YKKSEKKLIKDLKR 277 topA 3 YKKFKKKLLKSLKR 16 10; Conservative 58.6%; 71.4%; Score 51; DB Pred. No. 6.6; Mismatches 2; 2 Length 487; Indels 0; Gaps 0; GB: AE00

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RESULT 3
H75179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PAB2413 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
C;Accession: H75179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: Pyrococcus abyssi genome sequence: A;Reference number: A75001
A;Accession: H75179
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C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: A non-canonical genetic code in an early diverging eukaryotic lineage. A;Reference number: S70634; MUID:96208514; PMID:8641293
A;Accession: S70634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Hexamita sp.
A;Variety: ATCC 50330
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change C;Accession: S70634
R;Keeling, P.J.; Doolittle, W.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: PABA413
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-139 <KAW>
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hypothetical protein orf472 [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U29442; NID:g1322215; PIDN:AAC47211.1; PID:g1322216 A;Experimental source: ATCC 50330
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-399 < KEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Keeling, P.J.; Doolittle, W.F. EMBO J. 15, 2285-2290, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49519.1; PID:g54580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, July 1999
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                                                                 в90095
                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                  A; Genetic code: SGC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation elongation factor eEF-1 alpha chain - Hexamita sp. (strain ATCC 50330) (frac
                                                                                    RESULT 5
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                                                                                                                                                                                                                                                                                                          Superfamily: translation elongation factor Tu; translation elongation factor Tu homoly; Keywords: GTP binding; protein biosynthesis
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les 8; Conserv
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                                                                                                                                                                                       1 ALYKKFKKKLLKSLKRLG 18
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9; Conser
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8; Conserv
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44.4%;
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                                                                                                                                                                                                                                                    Score 46; DB Pred. No. 30;
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C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-472 < DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Douglas, S.; Zauner, Nature 410, 1091-1096,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-733 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                         A;Title: The complete primary structure of glycosylated A;Reference number: S69133; MUID:95255268; PMID:7737160 A;Accession: S69133
                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein
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          C; Superfamily: beta-thromboglobulin
                             A; Note: blocked N-terminus
                                                A; Molecule type: protein A; Residues: 1-90 < PRO>
                                                                                      A; Status: preliminary
                                                                                                                                                                                                       C; Accession: S69133
                                                                                                                                                                                                                                                                      platelet factor 4 -
                                                                                                                                                                                                                                                                                              S69133
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A;Cross-references: GB:AF165818; NID:g13794515; PIDN:AAK39890.1; GSPDB:GN00150 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 C:Accession: B90095
                                                                                         platelet factor 4 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z25022
A; Accession: T49679
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C;Accession: T49679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable branching enzyme (bel) [imported] - Neurospora crassa N; \texttt{Alternate} names: protein \texttt{B8B20.330}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 30/2; 74/3; 108/1; 146/3; 377/2; 489/2; C;Superfamily: 1,4-alpha-glucan branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Neurospora crassa
               R;Proudfoot, A.E.I.; Magnenat, E.; Haley, T.M.; Maione, T.E.; Wells, T.N.C. Eur. J. Biochem. 228, 658-664, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.330
                                                                                                                                                                                                                                                                      220 ATYKEFTKTMLPRIKNLG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%;
                                                                                                                                                                                                                                                                                                                                                                                             52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone B8B20; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome of an enslaved algal nucleus MUID:11323671; PMID:11323671
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2; Pred. No. 53;
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35;
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porcine platelet factor 4.
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RESULT 10
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A; Introns: 22/3; 36/1; 75/3; 136/2
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                                                                                                                                                                                                                                                                                                                                             A;Accession: T33883;
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-160 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                R:Becker, M.; Wamsley, P.; Twyman, B.; Beck, C.; Bradshaw, submitted to the EMBL Data Library, February 1999 A;Description: The sequence of C. elegans cosmid H14E04. A;Reference number: Z21431
                                                                                                                                                                                                                                                                 A; Gene: CESP:H14E04.4
                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF125448; PIDN:AAD12811.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein H14E04.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.; Ohfuku, Y.; Funchashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Rushida, W.; Oyuci DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
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A; Residues: 1-140 <KAW>
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M.; OhfuKu, Y.; Funehashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PH1560 - Pyrococcus horikoshii C:Species: Pyrococcus horikoshii
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                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T33883
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                                                      111 FONESKKELKNLKNEG 126
                                                                                                                                         Local Similarity les 8; Conserv
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                                                                                             3 YKKFKKKLLKSLKRLG 18
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                                                                                                                                         Conservative
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50.0%;
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83.3%;
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                                                                                                                                       ω
                                                                                                                                                        Score 45;
Pred. No.
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                      N2; clone H14E04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
11;
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                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ν,
                                                                                                                                                                                                                                                                                                                         ,GSPDB:GN00022; CESP:H14E04.4
                                                                                                                                                                            Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                Gaps
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                                                                                                                                0;
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      JC5923
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AH1489

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В
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S38002; S44589; S38499
R;Vandenbol, M.; Bolle, p.A.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37976
                                                                                                                                                                                                                                       A; Map position: 11L
                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z26878; NID:g407503; PIDN:CAA81515.1; PID:g407510
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-427 < V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A: Title: Sequencing and analysis of a 20.5 kb DNA segment located on the left arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F. Yeast 10, 25-33, 1994
RESULT
                                                                                                                                                                                                                                                              A; Cross-references: SGD:S0001655
                                                                                                                                                                                                                                                                                        A; Gene: SGD: EBP2
                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S44583
A; Accession: S44589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: 228172; NID: g486301; PIDN: CAA82014.1; PID: g486302; MIPS: YKL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-427 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein YKL172w - yeast (Saccharomyces cerevisiae) N:Alternate names: hypothetical protein YKL636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S38002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL592022; PIDN:CAC95688.1; PID:g16412897; GSPDB:GN00178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294, 849-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; Dominguez-Bernal,
                                                                                                                                                    Matches
                                                                                                                                                                                           Query Match
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Best Local :
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                                                              75 ALSKKEKRKLKKELKKM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 LYRKFRKRLVNNYKK 185
                                                                                                                                                                      Local Similarity
                                                                                                     1 ALYKKFKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LYKKFKKKLLKSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lin0456
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                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                       1-427 <VA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
                                                                                                                                                                      51.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.7%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
                                                                                                                                               Mismatches
                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45;
Pred. No.
                                                                                                                                                                                      Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
21;
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                                                                                                                                                                                      Length 427;
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                                                                                                                                               0
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                                                                                                                                          Gaps
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glutamate-tRNA ligase (EC 6.1.1.17) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002
C;Accession: S51685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
S51685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: lyase
F;42-60/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AF036894; NID:g2906010; PIDN:AAC03768.1; PID:g2906011 C;Comment: This enzyme catalyzes the breakdown of sphingosine-1-phosphate which participes.
                                                                                                                         A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: E86212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X83524; NID:g603866; PIDN:CAA58506.1; PID:g603867 C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
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                                                                                                                                                                                                                                                                                                        R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-569 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S51684
A; Accession: S51685
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                                                                                              A; Reference number: A86141; A; Accession: E86212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Andersen, R.V.
                     A; Molecule type: DNA
A; Residues: 1-615 <STO>
                                                                        A; Status: preliminary
A;Cross-references: GB:AE005172; NID:g8439895; PIDN:AAF75081.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: sphingosine-1-phosphate lyase;Keywords: lyase
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Pred. No. 59;
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pyruvate kinase (EC 2.7.1.40) - Spiroplasma citri (fragment)
C;Species: Spiroplasma citri
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 07-Dec-1999
C;Accession: F35270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                             A;Genetic code: SGC3
C;Superfamily: pyruvate kinase
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-192 <CHE>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                         A;Reference number: A35270; MUID:90236934; PMID:2139649 A;Accession: F35270
                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: F35270
R;Chevalier, C.; Saillard, C.; Bove, J.M.
J. Bacteriol. 172, 2693-2703, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 1 C;Superfamily: tomato leucine zipper-containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Organization and nucleotide sequences of the Spiroplasma citri genes for rib
                                                                        B
                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                 Search completed: December 24, 2002, 09:20:06
 Job time :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 IYKKFRKKIIVDTLSHLG 216
                                                                        121 LSKKTKKQLLKIVKKL 136
                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LYKKFKKKLL-KSLKRLG 18
                                                                                                          2 LYKKFKKKLLKSLKRL 17
58 secs
                                                                                                                                              10;
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.1%;
50.0%;
                                                                                                                                                                50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44.5;
Pred. No. 7
                                                                                                                                                                Score 44;
Pred. No.
                                                                                                                                                Mismatches
                                                                                                                                                            DB
30;
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                                                                                                                                                                               Length 192;
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OM protein - protein search, using sw model
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December 24, 2002, 09:16:50 ; Search time 11 Seconds (without alignments) 67.870 Million cell updates/sec

Title: Perfect score: US-09-648-816B-3 87

1 ALYKKFKKKLLKSLKRLG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 112892

112892 segs, 41476328 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33	32	J.	ى د ت د	2 4) N	2 6 7	0 0) C) K) <u>(</u>	22	2	20) 19	81	10	10	7.5	14	1.	12	11	10	ı V	00	7	١٥	·	4.1	ندا -	ν.) <u> </u>	NO.	Result
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39255 bac	06227 hacteri	. mus	5230 oryc	bos taur	9055 archaeogl	308	a	149 saccha	233	saccharomy	5 bacillus s	2 buchnera	N	rattu	5 homo sapi	l aquif	51	5 saccharomy	9 bacillu	2 rattus nor	7	P51686 homo sapien	8060	9746 s	43585 sacch	247 h	9680 spiroplasm	3794 nicotiana	36049 saccharom	30034 sús scrofa	66893 aquifex ae	8759 methanoco	Description	

40 46.0 340 1 YC47_HELPJ 40 46.0 340 1 YC47_HELPJ 40 46.0 340 1 YC47_HELPJ 40 46.0 359 1 AG2S_HUMAN 40 46.0 359 1 CNA1_YEAST 40 46.0 369 1 CNA1_YEAST 40 46.0 413 1 GAG2_HUMAN 40 46.0 425 1 RHG8_MOUSE 40 46.0 425 1 RHG8_BUCAP 40 46.0 1202 1 YE01_SCHPO 40 46.0 1202 1 YE01_SCHPO 40 46.0 4427 1 PKSL_BACSU 39 44.8 54 1 STP1_MOUSE 39 44.8 55 1 PLF4_SHEEP
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1 YC47 HELPJ 1 YC47_HELPJ 1 YC47_HELPY 1 AG2S_HUMAN 1 CNA1 YEAST 1 GAG2_HUMAN 1 RHG8_MOUSE 1 RPOB_ASTLO 1 YE01_SCHPO 1 YE01_SCHPO 1 YE01_SCHPO 1 STPL_MOUSE 1 PLF4_SHEEP
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ALIGNMENTS

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TIGR; MJ1364; InterPro; IPR001656; UPF0024. Pfam; PF01142; UPF0024; 1. PROSITE; PS01268; UPF0024; 1. Hypothetical protein; Complete SEQUENCE 487 AA; 57426 MW;		or send an email to license	modified and this statement	use	between		-!- SIMILARITY: BELONGS T	Extra Science 273:1058-1073(1996).	"Comprete genome sequence	Klenk HP., Fraser C.M.,		Utterback T	Scott J.L., Geoghagen	Overbeek R., Kirkness				STRAIN=JAL-1 / DSM 2661 / ATCC		N [1]				MJ1364.	Hypothetical protein MJ136	16 COM 2001 (NCL. 35, EdSt.	01-NOV-1997 (Rel. 35, Crea	(20/24)	YD64_METJA STANDARD;	RESULT 1 YD64_METJA
proteome. 1D8F68F634630604 CRC64;		@isb-sib.ch).	e by and for commerc	by non-profit institutions as long as its content is in no way	the Swiss Institute of Bioinformatics and the EMBL outstation		PF0024 FAMILY.		of the methanogenic archaeon, Methanococcus	H.O., Woese C.R., Venter J.C.;	, Kaine	Terson J.D., Sadow P.W., Hanna M.C.,		, ب	, CI	Zhou L., Fleischmann R.D.,		43067:			indococcus.	COCCi; Methanococcales;			annotation update) 4.	sequence update)			PRT; 487 AA.	

RESULT 2

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||| :|||:| ||| 264 YKKSEKKLIKDLKR 277 3 YKKFKKKLLKSLKR 16 Query Match
Best Local Similarity
Matches 10; Conserv

Conservative

58.6%; Score 51; D 71.4%; Pred. No. 2;

DB 1; Length 487; 2; Indels

2; Mismatches

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TOP1_AQUAE

TOP1_AQUAE

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AC 06893

DT 30-MAY

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OS Aquife

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                                                 RESULT 3
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aguifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   066893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1Ac; 1.
SMART; SM00436; TOP1Bc; 1.
SMART; SM00493; TOPRIM; 1.
TIGRFAMS; TIGRO1051; topA_bact; 1.
PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
-i- CATALYTIC ACTIVITY: ATP-Independent breakage of single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 392:353-358(1998)
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PLF4_PIG
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                                                                                                                                                                                            2 LYKKFKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, I WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOS AT ONE END OF THE ENZYME'S SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA, followed by passage and rejoining.
SUBUNIT: MONOMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                      Conservative
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DNAtopI_DNA_bind.
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     PRT;
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     90 AA
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       EBP2_YEAST
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Best Local :
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01-OCT-1994 (Rel.
15-JUN-2002 (Rel.
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01-JUN-1994
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CONFLICT
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Shigeta O., Lu W., Holt J.C., Edmunds L.H. Jr., Niewiarowski S.;
"Oyine platelet factor 4: purification, amino acid sequence,
radioimmunoassay and comparison with platelet factor 4 of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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HSSP; P02777; 1PLF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95255268; PubMed=7737160;
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                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
rRNA processing protein EBP2 (EBNA1-binding p
EBP2 OR YKL172W OR YKL636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00199; SCY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 LYKKIIKKLLKS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TORDS. Res. 64:509-520(1991).

FUNCTION: PLATELET FACTOR 4, NONCOVALENTLY BOUND TO A PROTEOGLYCAN MOLECULE, IS RELEASED DURING PLATELET AGGREGATION. PF4 NEUTRALIZES THE ANTICOAGULANT EFFECT OF HEPARIN BECAUSE IT BINDS MORE STRONGLY TO HEPARIN THAN TO THE CHONDROITIN-4-SULFATE CHAINS OF THE CARRIER MOLECULE. CHEMOTACTIC FOR NEUTROPHILS AND MONOCYTES.

SUBUNIT: HOMOTETRAMER.

SUBUNIT: HOMOTETRAMER.

PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE.

MODDIFIED WITH SIALIC ACID RESIDUES (MICROHETEROGENEITY).

SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE SIMULARITY: BELONGS TO THE TAKEN SIMULARITY: BELONGS TO THE TAKEN SIMULARITY SIMULARITY SIMULARITY: BELONGS TO THE TAKEN SIMULARITY SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001089; CXC_chmkine_smll
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Fungi;
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25
27
43
85
                                                                                                                                                                                                                                                                                   STANDARD;
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30, Last sequence update)
41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMALLCYTKCXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMALL_CYTOKINES_CXC; 1.
SMALL_CYTOKINES_CXC; 1.
Comparing the motion of the comparing of the comparing action of the comparing
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       Ascomycota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
67
43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemokine_IL8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQ -> PE (IN REF. 2).
108F15AC828FDE6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
E -> I (IN REF
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                                                                                                                                                                                                                                                                                      PRT;
       Saccharomycotina; Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> I (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                          yeast)
                                                                                                                                                                                                                                                                                          427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DΒ
                                                                                                           protein homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 90;
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                                                                                                                              RESULT 5
SYE_TOBAC
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                                                                                                                                                                                                                                                                   Query Match
                                                         SYE_TOBAC
Q43794;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
    Nicotiana tabacum (Common Eukaryota; Viridiplantae;
                                           Glutamyl-tRNA synthetase (EC
                                  (GluRS)
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                      Ribosome biogenesis: Nuclear protein; Coiled coil.

DOMAIN 45 174 COILED COIL (POTENTIAL).

DOMAIN 234 265 COILED COIL (POTENTIAL).

DOMAIN 291 348 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z26878; CAA81515.1; -.
EMBL; Z28172; CAA82014.1; -.
PIR; S38002; S38020.
PIR; S38409; S38409.
PIR; S384589; S44589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contribes requires a licenomial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         processing.";
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Ebp2p, yeast homologue of a human protein that interacts with Epstein Barr virus nuclear antigen 1, is required for pre-rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION, AND SUBCELLULAR LOCATION PubMed=10947841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilger "Sequencing and analysis of a 20.5 kb DNA segment located arm of yeast chromosome XI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The budding yeast homolog of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huber M.D., Dworet J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10849420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  processing and ribosomal subunit assembly.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsujii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast 10:S25-S33(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94378719; PubMed=8091858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales;
                                                                                                                                                                                    75
                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE EBP2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Required for the processing of the 279 Probably involved in the step of the processing precursor into the 27 SB intermediate. SUBCELLULAR LOCATION: Nuclear; nucleolar.
                                                                                                                                                                                  ALSKKEKRKLKKELKKM
                                                                                                                                                                                                            ALYKKFKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                   S0001655; EBP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cells 5:543-553(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R., Miyoshi K., Tsuno A., Matsui Y.,
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dding yeast homolog of the human EBNA1-binding protein is an essential nucleolar protein required for pre-rR
                                                                                                                                                                                                                                                                                          291
427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND SUBCELLULAR LOCATION.
                                                         (Rel.
                                                                                  (Rel.
                                                                                                                                                                                                                                        Conservative
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275:28764-28773(2000)
                                                                                                                                                                                                                                                                                             49734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                   51.7%;
58.8%;
                                                      Last sequence update)
                                                                                     Created)
Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shire K.,
                 tobacco)
                                                                                                                                                                                                                                        ω
••
                                        6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                   Score 45; DB
Pred. No. 14;
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                            4A11F6CDF779DB5A CRC64;
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                569 AA
                                                        update)
                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                             Length 427;
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Best Local
Le Dantec L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
-!- COFACTOR: REQUIRES MACMESIUM AND POTASSIUM.
-!- PATHWAY: Glycolysis; final step.
                                                                                                                                                                                                                                                                                                                                                                                                                                          _SPICI
                                                                                                                                                                                                                                                                                                                                         P19680: 030600;
01-FEB-1991 (Rel. 17, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pyruvate kinase (EC 2.7.1.40) (PK) (Fragment)
                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 27556 / R8A2;
MEDLINE=90236934; PubMed=2139649;
                                                                                                                          "Organization and nucleotide sequences of the Spiroplasma citri genes for ribosomal protein S2, elongation factor Ts, spiralin, phosphofructokinase, pyruvate kinase, and an unidentified protein."; J. Bacteriol. 172:2693-2703(1990).
                                                                                                                                                                                           Chevalier C.,
                                                                                                                                                                                                                                                                                   Spiroplasmataceae;
                                                                                                                                                                                                                                                                                                                 Spiroplasma citri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SITE 62 72 "HIGH" REGION.
SITE 303 307 "KMSKS" REGION.
BINDING 306 306 ATP (BY SIMILARITY).
SEQUENCE 569 AA; 63338 MW; F2E81D7346OA1844 CRC64;
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=2133;
                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                            KPY1_SPICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO0464; gltx_bact; 1.
PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X83524; CAA58506.1; -. HSSP; P27000; 1GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases -i- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_1c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diphosphate + L-glutamyi-trna(Glu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 ALYKQFAEKLLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                           Saillard C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  profit
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRNASYNTHGLU
                                                                                                                                                                                                                                                                                   Spiroplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%;
69.2%;
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                                                                                                                                                                                          Bove J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB
Pred. No. 19;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                 Entomoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                         192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
19;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           015247; 015174;
15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chloride intracellular channel protein 2 (XAP121).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Kinase; Glycolysis; Multigene family; Magnesium;
Transferase; Kinase; Glycolysis; Multigene family; Magnesium;
CONFLICT 82 192 HWRIKGLLOKSLUTYHOMNUNSIMFSPSFKFKHHYYTLLLS
CONFLICT 82 192 KYTKKOLLKIVKKLKKLOSOHYNLAHGLRETWTSSFCFNER
PSIMRILSSFKOIVFSFKISLVSKVLIKL -> RAGIMKGG
PKOEIVAGATVTIYSLPTEYQNREGTGTEITYSYDMSODLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD001009; Pyruvate_kinase; 1.
PROSITE; PS00110; PYRUVATE_KINASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 45:224-228(1997).
-i- FUNCTION: Possible chloride ion channel.
-i- TISSUE SPECIFICITY: EXPRESSED IN FETAL LIVER AND ADULT SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97480736; PubMed=9339381;
Heiss N.S., Poustka A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLI2_HUMAN
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Pfam; PF00224; PK; 1.
                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CLIC FAMILY OF CHLORIDE CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic structure of a novel chloride channel gene, CLIC2, in Xq28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                          Genew;
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300138;
                                                                                                                                         Y12696; CAA73228.1;
                          HGNC:2063;
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22209 MW;
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RESULT 8
YFA4_YEAST
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Best Local Similarity
'-has 9; Conserve
              Query Match
Best Local Similarity
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01-NOV-1995
15-JUN-2002
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P43585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ionic channel; Ion transport; Voltage-gated channel.
CONFLICT 109 109 S -> C (IN REF. 1; CAA03948).
CONFLICT 164 164 G -> E (IN REF. 1; CAA03948).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002946; Int_Cl_channel.
PRINTS; PR01263; INTCLCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95400292; PubMed-7670463;
MUTAKAMI Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00862; O-ClC; 1.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96381249; PubMed=8789262;
Naitou M., Ozawa M., Sasanuma S.-I.,
Shibata T., Hanaoka F., Watanabe K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFL004W.
                                                                        InterPro; 1100-1105; SPX; 1. Pfam; PF03105; SPX; 1. Hypothetical protein; Transmembrane. POTENT: 728 748 POTENT:
                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                 Yeast 12:77-84(1996)
                                                                                                                                                                                                                                                                                                           "Sequencing of a 23 kb fragment from Saccharomyces cerevisiae chromosome VI.";
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                       SEQUENCE
                                                                                                                                      SGD;
                                                                                                                                                 EMBL; D50617; BAA09234.1;
                                                                                                                                                                                                                                                                                    -!- SIMILARITY: TO YEAST YJL012C.
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                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KKFKKKLLKSLKRL 17
                                                                                                                                      S0001890;
 9;
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243 AA;
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1 95.4
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                                                       828 AA;
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Conservative
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                                                                                                                                       PHM
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32, Last sequence update)
41, Last annotation updat
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27812 MW;
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                                                     95440 MW;
              50.6%;
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              Pred. No. 38;
                          Score 44;
                                                                     POTENTIAL
                                                                                 POTENTIAL.
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                                                       BCEF34FDB2012ABD CRC64;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                       Ono A., Yamazaki M., Tashiro H.,
                                                                                                                                                                                                                                                                                                                                                                     Kobayashi M., Hagiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             828 AA
                               DB
                               1;
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                             Length 828;
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Matches

Qγ В

4

357

KKFKEQTLKKLKESG KKFKKKLLKSLKRLG

371 18

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YB65
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dagar R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dagar R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paussen I., Potashkin J.,
The genome sequence of Schizosaccharomyces pombe.";
RT The genome sequence of Schizosaccharomyces pombe.";
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01-NOV-1995 (Rel. 32, Last se
01-NOV-1995 (Rel. 41, Last a
                                        Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00611; FCH; 1.
                                                                                                                                                                                                                                                                                                                       the
                                                                                                        InterPro; IPR001452;
                                                                                                                        InterPro; IPR002219; DAG_PE-bind
                                                                                                                                                                       EMBL; Z54140; CAA90818.1; HSSP; P29354; 1GFC.
                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein C12C2.05c in chromosome SPBC12C2.05C.
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                                                                                                                                              InterPro; IPR001060; Cdc15_Fes_CIP4.
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                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING DOMAIN.
SIMILARITY: CONTAINS 1 FCH DOMAIN.
SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO YEAST BZZ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHPO
                                                                                    PF00018; SH3;
PD000066;
                 PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                        SH3.
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                                                                                                                                                                                                                                                                       MEDLINE-9928/316; PubMed=10360571; Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Melson K.E., Clayton R.A., Gill S.R., Melson W.C., Ketchum K.A., Haft D.H., Hickey E.K., Petterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from "Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P50908;
01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sterner R., Dahm A., Darimont B., Ivens A., Liebl W., Kirschner I "(Beta alpha)8-barrel proteins of tryptophan biosynthesis in the hyperthermophile Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P50908;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00109; C1; 1.
SMART; SM00055; FCH; 1.
SMART; SM00326; SH3; 2.
                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                            genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 14:4395-4402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tryptophan synthase alpha chain (EC TRPA OR TM0137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRPA_THEMA
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PROSITE; PS50002; SH3; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00479; DAG_PE_BIND_DOM_1; PROSITE; PS50081; DAG_PE_BIND_DOM_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96003619; PubMed=7556082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LYKKF---KKKLLKSLKR 16
                                                                                           SIMILARITY).
SIMILARITY: BELONGS TO THE TRPA FAMILY.
                                                                                                                          - L-tryptophan + glyceraldehyde 3-phosphate + H(2)0.
PATHWAY: Tryptophan biosynthesis; fifth (last) step.
SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (
                                                                                                                                                                          CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
                                                                                                                                                                                                           FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE OF INDOLEGLYCEROL PHOSPHATE TO INDOLE AND GLYCERALDEHYDE 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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190
447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
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Best Local
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P51686;
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InterPro: IPR002028; Trp_synthaseA.
Pfam; PF00290; trp_Syntha; 1.
ProDom; PD001335; Trp_synthaseA; 1.
PTGREAMs; TTGR00262; trpA; 1.
PROSITE; PS00167; TRP_SYNTHASE_ALPHA; 1.
PROSITE; PS00167; TRP_SYNTHASE_ALPHA; 1.
PROSITE; PS00167; TRP_SYNTHASE, Complete proteome.
Tryptophan biosynthesis; Lyase; Complete proteome.
CONFLICT 189 189 F -> L (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        -i- FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HV-1 infection.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9) (GPR-9-
                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE=99248139; PubMed=10229797;
Zaballos A., Gutierrez J., Varona R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                 receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                     ZADALIOS A., Gutlerrez J., Varona R., Ardavin C., Marquez "Identification of the orphan chemokine receptor GPR-9-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Lautens L.L., Tiffany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCR9 OR CMKBR9
InterPro;
                  InterPro;
                                     MIM; 604738;
                                                      Genew;
                                                                       EMBL; U45982;
                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 YPEGKEKLLDELKKLG 106
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P00929; 2WSY.
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                                                     HGNC:1610; CCR9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
 IPR000276;
                    IPR004069;
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                                                                       AAA93319.1;
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 GPCR_Rhodpsn
                    CC_chemkine9
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Ardavin C.,
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16;
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CKR9_MOUSE
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20069400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCR9 OR CMKBR10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
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73
94
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Q9WUT7;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)
(Chemokine C-C receptor 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01531; CHEMOKINER9.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                       Wurbel M.A., Philippe J.M., Nguyen C., Victorero G., Freeman Wooding P., Miazek A., Mattei M.G., Malissen M., Jordan B.R., Malissen B., Carrier A., Naquet P.;
"The chemokine TECK is expressed by thymic and intestinal epi
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Thymus;
MEDLINE=99248139; PubMed=10229797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
-i- SUBCELLULAR LOCATION: Integral membrane
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN
-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PRO-
                                                                                                                                                                    cells and attracts double- and single-positive the TECK receptor CCR9.";
                                                                                                                                                                                                                                                                                                                                                     Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.; "Cutting edge: identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK."; J. Immunol. 162:5671-5675(1999).
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37 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                 PubMed=10602049;
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Pred. No.
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (
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3 (POTENTIAL)
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    COUPLED
                                                                                                                                                                                                                                                         Jordan B.R.,
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RESULT 13
KP58_RAT
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Best Local
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                                 Kerr M., Fischer J.E., Purushotham K.R., Gao D., Nakagawa Y., Maeda N., Ghanta V., Hiramoto R., Chegini N., Humphreys-Beher M.G. "Charracterization of the Synthesis and expression of the GTA kinas from transformed and normal rodent cells.", Biophys. Acta 1218:375-387(1994).
                                                                                                                                                                                                                                  01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Sal
MEDLINE=94325346; PubMed=8049264;
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                   Galactosyltransferase associated protein kinase P58/GTA (EC
                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                         P46892;
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                       KP58_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1341902; Cmkbr10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                    322 ERFRRDLVKTLKNLG 336
                                                                                                                                                                                                                                                                                                                                                                             4 KKFKKKLLKSLKRLG 18
        FUNCTION: ACTS AS A NEGATIVE REGULATOR OF THE NORMAL CELL PROGRESSION. IN VITRO, THIS PROTEIN KINASE HAS BEEN SHOWN
PHOSPHORYLATE A NUMBER OF SUBSTRATES,
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38,
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                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                             TISSUE=Salivary gland;
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CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
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7 (POTENTIAL).
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2 (POTENTIAL).
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3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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INCLUDING
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HISTONE
                                                             the GTA-kinase
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                                                                                                                                                                                                                                                                                                                                                                                                             DHAL_BACST
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                               Imanaka T., Ohta T., Sakoda H., Widhyastuti N., Matsuoka M.;
"Cloning, nucleotide sequence, and efficient expression of the gene
coding for thermostable aldehyde dehydrogenase from Bacillus
stearothermophilus, and characterization of the enzyme."

J. Ferment. Bioeng. 76:161-167(1993)

-i- FUNCTION: OXIDIZES SEVERAL ALIPHATIC ALDEHYDES, PARTICULARLY C6-
ALIPHATIC ALDEHYDE AND HEXANAL, BUT DO NOT OXIDIZE BENZALDEHYDE.

THE OPTIMUM TEMPERATURE IS AROUND 55 AND 60 DEGREES CELSIUS.

-i- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)0 = an acid + NAD
-i- COFFACTOR: REQUIRES EITHER NAD OR NADP AS A COENZYME.
                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
BINDING
ACT_SITE
    -!- PATHWAY: Ethanol utilization; second step.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                            STRAIN-SIC1;
                                                                                                                                                                                                                                                                                                                                                                                             DHAL_BACST
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                  Aldehyde dehydrogenase, thermostable
                                                                                                                                                                                                                                                                                                                                                                                P42329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Euk_pkinase; 1 SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interPro; IPR002290; Ser_thr_pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L24388; AAA88509.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 KKNRKKLVKGLHRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 KKFKKKLLKSLKRLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC, NUCLEAR AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CASEIN, AND GALACTOSYLTRANSFERASE. MAY FUNCTION IN REGULATING PROLIFERATION BY THE PHOSPHORYLATION AND SUBSEQUENT PLASMA MEMBRANE TARGETING OF GALACTOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRANES
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203
436
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25 30 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
30 44 CALMODULIN-BINDING (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
49547
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364
93
108
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60.0%;
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                                                                                                                                                                                                                                                                     Bacillales; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D2BA9BC73EAD3D27 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                             update)
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(EC 1.2.1.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 436
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GLGB_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                          STRAIN-S288c / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.
Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         "Coordinate regulation of glycogen metabolism in the yeast Saccharomyces cerevisiae. Induction of glycogen branching enzyme."; J. Biol. Chem. 267:15224-15228(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P32775;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=92340578; PubMed=1634552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,4-alpha-glucan branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLGB_YEAST
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;

    -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 VYEPFKAKLLERVKQL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LYKKFKKKLLKSLKRL
                                                                    PATHWAY: Glycogen biosynthesis; third step.
DEVELOPMENTAL STAGE: EXPRESSED DURING THE TRANSITION BETWEEN THE
LATE EXPONENTIAL AND STATIONARY GROWTH PHASES, COINCIDENT WITH
MAXIMAL GLYCOGEN ACCUMULATION.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                            glycogen.
                                                       KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             V.J., Vigneron-Lesens C., Marianne-Pepin T., A., Rachez C., Ball S.G., Cannon J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR YEL011W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D13846; BAA02975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P51977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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    Last sequence update)
    Last annotation update)
    branching enzyme (EC 2.4.1.18) (Glycogen branching

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255 E
289 E
52915 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
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BY SIMILARITY.
BY SIMILARITY.
29E824451985D9ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
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Cherry J.M.,
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DЬ
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                                                Matches
                                                           Query Match
Best Local :
                                                                                                                          Glycogen |
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                 PIR;
SGD;
                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                               Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase_N; 1.
                                                                                                                                                                                                                                                         EMBL; M76739; AAA34632.1; -. EMBL; U18530; AAB64488.1; -.
                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                   SEQUENCE
                                                                                                                CONFLICT
                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                     InterPro; IPR000461; Alpha_amylase
213 YKEFTEKVLPRIKYLG 228
                        3 YKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                 A42752; A42752
S0000737; GLC3
                                               Similarity
8; Conserv
                                                                                                                                       biosynthesis; Transferase; Glycosyltransferase.
356 356 BY SIMILARITY.
417 417 BY SIMILARITY.
                                                                                                                                                                                                       IPR004193;
                                                                                                   704 AA;
                                                                                                                486
564
                                                Conservative
                                                                                                 356
417
486
564
81115 MW;
                                                                                                                                                                                                          Isoamylase_N.
                                                             48.3%;
50.0%;
                                                             Score 42;
Pred. No.
                                                                                                                BY SIMILARITY.
S -> T (IN REF.
                                                                                                    9C227E107B825F27 CRC64;
                                                Mismatches
                                                               DB 1;
65;
                                                                         Length 704;
                                                   Indels
                                                   0;
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Search completed: December 24, 2002, 09:18:46
Job time : 14 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
Sequence:
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SPTREMBL_21:*

Sp_archea:*

Sp_bacteria

sp_bacteria

sp_fungi:*

sp_human:*

sp_invert

sp_invert

sp_manmal

sp_marmal

sp_rorga

sp_pac

sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-648-816B-3
87
1 ALYKKFKKKLLKSI.K
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         sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                               sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_invertebrate:*
sp_mammal:*
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                                                                                                                                                                                               sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length DB	B	ID	Description
۲	47	54.0	139	17	Q9V132	09v132 pvrococcus
2	46	52.9	215	2	Q9Z655	092655
ω	46	52.9	399	C1	025166	025166
4	46	52.9	472	2	098R07	Cipacilità Doscas
S.	46	52.9	741	ا بن	242460	round Abroad
6	45	51.7	75	5	099245	prodection adapta
7	45	51.7	140	17	059212	059313 BURGAGANA
80	45	51.7	160	U	Q9TYP3	Spanoration Edution
9	45	51.7	187	16	092EK3	090bk3 listoria i
10	45	51.7	248	11	09D423	09473
11	45	51.7	568	11	054955	054055
12	45	51.7	568	11	08R0X7	0870×7
13	45	51.7	4146	J S	Q9DEI1	09dei1
14	45	51.7	6885	4	OHXW8O	rejues omou Odxago
15	44.5	51.1	615	10	640T60	09lang arahidonsis
16	44		246	16	Q8RA17	Q8ra17 thermoanae

RESULT 2 Q9Z655

45	. 4	43	42	41	40	w 9	ω 8	37	36	ယ	34	ω	32	3 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17
42	42	42	42	42	42	42	42	42	42	42.5	43	43	43	43	43	43	43	43.5	44	44	44	44	44	44	44	44	44	44
48.3	48.3	48.3					48.3	48.3	48.3	48.9	49.4	49.4	49.4	49.4	49.4					50.6							50.6	
558	427	427	427	427	420	369	218	175	145	141	727	497	477	460	439	398	139	69	841	778	729	531	511	460	437	266	254	247
10	16	16	N		11	4	16	16	N	12	16	16	16			σ		17	2	12	w	ഗ	5	12	12	17	α	4
Q9м175	034945	034491	088126	P97242	Q99LT9	Q9UQQ6	Q8RFB0	Q8XNU4	Q9AHW6	Q9YW61	Q8YZG7	Q99R73	Q8R6Z4	Q96Y49	Q53589	002339	Q8ZVC7	Q8TXT3	Q9AIP3	Q84509	074985	Q95xx1	Q8WTL1	041969	Q9QAH9	Q97YL4	Q98RW7	Q8TCE3
Q9m175 arabidopsis	-	$\mathbf{-}$		P97242 helicobacte	o	ゴ			0	Q9yw61 melanoplus			Q8r6z4 thermoanaer	Q96y49 sulfolobus		0		Q8txt3 methanopyru	1.2	9			0			4	quill	Q8tce3 homo sapien

ALIGNMENTS

ДЬ	Que Bes Mat	SQ					RT		RP	RN	0 x	8	88	O N	DE	DŢ	DT	DT	AC	IJ	RESULT 1
1 ALYKKEKKKLLKSLKRLG 18 : : :::: 60 SLYPKVSKKVLRALEOMG 77	Query Match 54.0%; Score 47; DB 17; Length 139; Best Local Similarity 44.4%; Pred. No. 23; Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;	Hypothetical protein; Complete proteome. SEQUENCE 139 AA; 16215 MW; 5B72C93C2398A060 CRC64;	SMART; SM00384; AT_hook; 1. TIGRFAMS; TIGR01199; HTH_fis; 1.	Pfam; PF02178; AT_hook; 1.	EMBL; AJ248284; CAB49519.1; InterPro: IPR000637: AT hook	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.	structure and evolution.";	300000 0000000000000000000000000000000	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=29292;	Pyrococcus.	arghaea: Eurvarchaeota: Thermococci: Thermococcaelor: Thormococcaelor.	PAB2413.	ical protein PAB2413	(TrEMBLrel. 21, Last	(TrEMBLrel. 13,	01-MAY-2000 (TremBLrel. 13, Created)		O9V132 PRELIMINARY: PRT: 139 AA	ЛТ 1

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RESULT
Q25166
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Q92655;
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Best Local
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InterPro; IPR004161; EFTU_D2.
InterPro; IPR00795; EF_GTPbind.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of 43A9 fosmid clone of Zymomonas mobilis ZM4."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF102543; AAD19422.1; -.
Hypothetical protein.
SEQUENCE 215 AA; 25210 MW; 48D3088672D9A05B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spironucleus barkhanus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ZM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96208514; PubMed=8641293; Keeling P.J., Doolittle W.F.; "A non-canonical genetic code in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=103874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae;
                                                                                                                                                                                                                                                        GTP-binding; Protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U29442; AAC47211.1; HSSP; P07157; IAIP.
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                                                                                                                                                                                       SEQUENCE
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148 ARYKEIKEEMQKNLKQIG 165
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                                           ALYKKFKKKLLKSLKRLG 18
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8; Conser
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399 AA;
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                                                                                            Conservative
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                                                                                                                                                                                    44204 MW;
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44.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46;
Pred. No.
                                                                                                                     Score 46; DB Pred. No. 80;
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                                                                                                                                                                                         2C46EA57A2B32E1E CRC64;
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                                                                                                                                           DB 5;
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                                                                                                                                           Length 399;
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RESULT 6
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 57.1 kDa protein orf472 from chromosome
ORF472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9P5P3;
Q9P5P3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Wu X., Reith M., Cavaller-Smith T., Maler U.G.; "The highly reduced genome of an enslaved algal nucleus."; Nature 410:1091-1096(2001).

EMBL; AF165818; AAK39890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98RQ7
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Probable branching enzyme (bel).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guillardia theta (Cryptomonas phi)
                                                                                                                                                                                                                                                                                                                                       German Neurospora genome project;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AL35593; CAB91480.2; -
Interpro; IPR004061; Alpha_amylase.
Interpro; IPR004193; Isoamylase_N.
Pfam; PF00128; alpha-amylase; 2.
Pfam; PF00128; alpha-amylase; 2.
Pfam; PF02922; isoamylase, 2.
SEQUENCE 741 AA; 84338 MW; E2F8CFA7B2FF1DF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 472 AA; 57116 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B8B20.330.
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                                                                                                                    216
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                                                                                                                  ATYKEFTKTMLPRIKNLG
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9; Conser
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9; Conserv
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                                                                                                                                                                                                                                                           52.9%;
50.0%;
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                                                                                                                                                                                                                              Score 46; DB 3; Lo
Pred. No. 1.4e+02;
""amatches 6;
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Pred. No.
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PRELIMINARY;

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Best Local Similarity
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01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                             InterPro; IPR000637; AT_hook.
Pfam; PF02178; AT_hook; 1.
SMART; SM00384; AT_hook; 1.
Hypothetical protein; Complet
SEQUENCE 140 AA; 16271 MW;
                                                                                                                                                                                                                                                     Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
                                                                                                                                                                                                           Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998
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EMBL; AE006577; AAK34220.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 75 AA; 8716 MW; 49A8B6063A7E91BC CRC64;
                                                                                                                                                                                                                                                                                                                               MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                  STRAIN-OT
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein PH1560
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE=21192684; pubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1314;
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                           1 ALYKKFKKKLLKSLKRLG 18
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SLYPKVSKKVMRALEQMG
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                                                                                                                                                                                  AP000006; BAA30672.1; -.
                                                                     Similarity
                                                                                                                                                                                                5:55-76(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                      Euryarchaeota; Thermococci;
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Gremblel.
Gremblel.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation undat
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16271 MW; 53E3820315634968 CRC64;
                                                                     51.7%;
38.9%;
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62.5%;
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                                                                 Score 45; DB 17;
Pred. No. 45;
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Pred. No.
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                                                      Mismatches
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Q1_DEC-2001 (TrEMBLrel. 19, Created)

Q1_DEC-2001 (TrEMBLrel. 19, Last sequence update)

Q1_MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Latster N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterstton R.,
Thierry Mieg J., Thomas K., Vaudin M., Waghan K., Waterstton R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M D of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                  PubMed=11679669;
                                SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / SEROVAR 6A;
                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales
Listeriaceae; Listeria.
                                                                                                                            Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becker M., Wamsley P., Twyman B., Beck C., Bradshaw H.; "The sequence of C. elegans cosmid H14E04."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                              NCBI_TaxID=1642;
                                                                                                                                             LIN0456
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF125448; AAD12811.1; -.
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
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 Frangeul L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             160 AA;
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Buchrieser C.,
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Rusniok C.,
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RESULT 10
Q9D423
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
                Query Match
Best Local
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4933421B21Rik protein.
4933421B21RIK.
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Hypothetical protein; Complete
SEQUENCE 187 AA; 22550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:849-852(2001).
EMBL; AL596165; CAC95688.1; -.
                                                                                           Nature 409:685-690(2001).
EMBL; AK016857; BAB30468.1; -.
MGD; MGI:1918324; 4933421B21R1K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001
                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 LYRKFRKRLVNNYKK 185
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                Similarity
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Conservative
                                                                           AA;
                                                                         29130 MW;
                51.7%;
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. 17, Last sequence. 17, Last annotation.
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                Score 45; DB
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome
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                                                                           F4F6108B0EB2654D CRC64;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
<del>ر.</del>
                                  Length 248;
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  Indels
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LYKKFKKKLLKSLKRLG

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Q8R0x7
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Best Local
                                                     Best Local Similarity Matches 7; Conser
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                               Q8ROX7 PRELIMINARY;
Q8ROX7;
Q1-JUN-2002 (TIEMBLIEL 21, C
01-JUN-2002 (TIEMBLIEL 21, L
01-JUN-2002 (TIEMBLIEL 21, L
Sphingosine phosphate lyase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          054955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ol-JUN-1998 (TERMBLIEL. 06, Created)
Ol-JUN-1998 (TERMBLIEL. 06, Last sequence update)
Ol-JUN-1998 (TERMBLIEL. 21, Last annotation update)
Sphingosine-1-phosphate lyase (EC 4.1.2.27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene and its functional expression in yeast ";
Biochem. Biophys. Res. Commun. 242:502-507(1998).
-:- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=98125521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00282; pyridoxal_deC; 1.
Decarboxylase; Lyase; Pyridoxal phosphate.
SEQUENCE 568 AA; 63707 MW; BA1852EFE42DF099 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1261415; Sgpll.
InterPro; IPR002129; Pyridoxal_deC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGPL1
                                                                                                             SEQUENCE
                                                                                                                                         Submitted (APR-2002) to the EMBL; BC026135; AAH26135.1;
                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of the first mammalian sphingosine phosphate lyase
                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                     TISSUE=LIVER;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                            yase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 LYHRYRRKCLSERKRLG 73
                                                                                                                                                                                                                                                                                                                                                                                                                            65 SLWSRFKKKLFKLIRKM 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 7; Conserv
65
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALYKKFKKKLLKSLKRL 17
                          1 ALYKKFKKKLLKSLKRL 17
SLWSRFKKKLFKLIRKM 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF036894; AAC03768.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saba J.D
                                                                                                             568 AA;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                     (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.7%;
41.2%;
                                                                                                             63677 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                   51.7%;
41.2%;
                                                                                                                                                        EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
                                                                   Pred. No. 1.5e+02;
                                                                               Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.
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                                                                                                              FA5D52E4E49DF09E CRC64;
                                                     Mismatches
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                                                                                                                                                                                                                                                                                                             sequence update)
                                                                                                                                                                                                                                                                                                 annotation
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                                                                                                                                                                                                                                                                                                                                                        568 AA
                                                                                    DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5e+02;
3;
                                                                                                                                                                                                                                                                                                update)
                                                                               Length 568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                           01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                     Pfam;
             Pfam; PF00810; ER_lumen_recept; 1.
Pfam; PF00435; spectrin; 14.
SMART; SM00033; CH; 2.
                                                               "NUANCE, a giant protein connecting nucleus and actin cytoskeleton.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435011; AA.133548.1; -
InterPro; IPR001589; Actbind_actnin.
InterPro; IPR000515; BPD_transp.
InterPro; IPR000515; BPD_transp.
InterPro; IPR000133; ERret_receptor.
InterPro; IPR000133; ERret_receptor.
InterPro; IPR00017; Spectrin.
                                                                                                                                                                                  Zhen
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                       Q8WXH0;
                                                                                                                                                                                                                                                                                                                                                                    OHXM8O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02259; FAT; 1.

Pfam; PF02260; FATC; 1.

Pfam; PF00454; PI3_P14_kinase; 1.

SMART; SM00146; PI3KC; 1.

PROSITE; PS00915; PI3_4_KINASE_1; UNKNOWN_1.

PROSITE; PS50290; PI3_4_KINASE_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09DELL:
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC tremburger kinase catalytic subunit.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawahara A., Tatsumi K., Abe M.; "Identification of four highly conserved regions in DNA-PKcs.", Immunogenetics 51:965-973(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujimori A., Araki R., Fukumura R., Ohhata T., Takahashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=J; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DEI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003152; FATC.
InterPro; IPR000403; PI3_PI4_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20456723; PubMed=11003390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB016434; BAA36690.1; -.
InterPro; IPR003151; FAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DEI1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         842 SLHKGFNKQLIQQLKRM 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKKFKKKLLKSLKRL 17
                                                        PF00307; CH; 2.
SM00033; CH; 2.
SM00150; SPEC; 20.
                                                                                                                                                                               Y., Libotte T., Noegel A.A.,
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2 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473496 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.7%;
47.1%;
                                                                                                                                                                                                                                                                                                     20, Created)
20, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB
Pred. No. 8.7e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C91F8BC517C7CBF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 6885 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4146 AA
                                                                                                                                                                               Korenbaum E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 8.7e+02;
cches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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B
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Q9LQP9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P., Toriumi M., Chin C., Choi E., Chiou J., Gonzalez A., Chung M., Howng B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A., "The sequence of BAC F24B9 from Arabidopsis thaliana chromosome 1.";
                                                                                                                                                                                                    Theologis A.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ EMBL; AC007583; AAF75081.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9LOP9

O9LOP9;

O1-OCT-2000 (TrEMBLrel. 15,

O1-OCT-2000 (TrEMBLrel. 15,

O1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                         PROSITE; PS00061; ADH_SHORT; UNKNOWN_1
                                                                                                                                                                                                                                                                                                    Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                        Pfam; PF03081; Exo70;
                                                                                                                                                                         InterPro; IPR002198; ADH_short.
InterPro; IPR004140; Exo70.
                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                          STRAIN=CV.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F24B9.17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS50021; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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199 IYKKFRKKIIVDTLSHLG
                             2 LYKKFKKKLL-KSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKKFKKK-----LLKSLKRLG 18
                                                               Similarity 9; Conserv
                                                                                                                          615 AA;
                                                                                                                                                                                                                                                       COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6885 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                               Conservative
                                                                                                                          68401 MW;
                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.7%;
52.2%;
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 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                         Score 44.5;
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Pred. No. 1.4e+03;
1; Mismatches 4
                                                                            Pred. No. 1.9e+02
                                                                                                                         02CAEBBE04448622 CRC64;
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         615
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                                                                                           DB 10;
                                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core eudicots; Rosidae;
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                                                          Gaps
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Search completed: December 24, 2002, 09:20:43 Job time : 33 secs

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Database
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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87
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                /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version
Copyright (c) 1993 - 2002
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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30.174 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	48.3	48.3	48.3	48.3	48.3	48	49.4	52.9	Maten	Query	ρ
867	690	203	172	145	101	70	70	13	13	13	1138	1004	357	357	357	108	439	46	Match Length		
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US-09-992-598-84	US-09-801-368-40	US-09-768-826-41	US-09-925-301-987	US-09-768-826-60	US-09-940-063-8	US-09-229-304-10	US-09-792-793A-91	US-10-036-869-9	US-09-925-715-27	US-09-765-614B-31	US-09-767-215-5	US-09-767-215-2	US-10-000-759A-2	US-09-952-385-2	US-09-903-377-2	US-09-822-263-14	US-09-815-242-5696	US-10-036-869-11	ID		
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
38	38	38	38.5	38.5	39		39	39	39	39	39.5	40	41	41	41	41	41	41	41	41	41	41	41	41	,
43.7		43.7	44.3	44.3	44.8	44.8	44.8	44.8	44.8	44.8	45.4	46.0	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	
29	17	17	1019	917	855	829	828	695	231	80	389	139	867	867	867	867	867	867	867	867	867	867	867	867	000
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US-09-872-864-19	US-09-554-000-39	US-09-999-745-55	US-09-801-574-76	US-09-808-743-10	US-09-792-127-4	US-09-792-127-5	US-08-681-219-28	US-09-792-127-2	US-09-828-644-105	US-09-916-790-10	US-09-835-788A-14	US-09-864-761-45901	US-09-989-721-84	US-09-990-456-84	US-09-993-604-84	US-09-991-163-84	US-09-990-442-84	US-09-991-073-84	US-09-989-732-84	US-09-989-731-84	US-09-989-727-84	US-09-989-279-84	US-09-989-723-84	US-09-989-722-84	00 00 000 01
e 19	Sequence 39, Appl	Sequence 55, Appl	76,	10,			Sequence 28, Appl	Sequence 2, Appli	Sequence 105, App	Sequence 10, Appl	Sequence 14, Appl	459	84,		-	Sequence 84, Appl	Sequence 84, Appl	84,	84,		Sequence 84, Appl	84,	Sequence 84, Appl	Sequence 84, Appl	Coduction of Dipt

ALIGNMENTS

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US-10-036-869-11
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                                                                                                                        INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-Wo. US/20020151516A1-2001
CLASSIFICATION: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mixson, James A
                                                                                                                                               TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/985,526 FILING DATE: <Unknown>
                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Connolly, Bove, Lodge, & Hutz STREET: 1220 Market Street, P.O. Box 2207
                              TOPOLOGY:
                                                                                                                                                                                                                     NAME: McMorrow Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Delaware
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                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Staphylococcus aureus US-09-815-242-5696
                                                                                                                                                                                                            US-09-822-263-14
                                 APPLICANT: Prayaga, Sudhirdas
APPLICANT: Vernet, Corine
APPLICANT: Shimkets, Richard A
APPLICANT: Burgess, Catherine
APPLICANT: Spytek, Kimberly
APPLICANT: Tchernev, Velizar T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5696, Application US/09815242 Patent No. US20020061569A1
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Best Local S
                                                                                                                                              Sequence 14, Application US/09822263 Patent No. US20020036598A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5696
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625
TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                       391 YAKFRDKILDKLEKMG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Karı L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto, Robert T
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 10; Length 439; Pred. No. 38;
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US-09-903-377-2
  B
                                                                                                                                                        US-09-903-377-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
TITLE OF INVENTION: RECEPTOR 9A GENE DISRUPTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14
                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 357
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PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/158,942
PRIOR FILING DATE: 1999-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/822,263
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/672.665
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/2 PRIOR FILING DATE: 2000-06-29
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PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/169, 344
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/221,483
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/262,113
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/217,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: R-365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                          OTHER INFORMATION: Targeting vector
                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                              FEATURE:
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310 ERFRRDLVKTLKNLG 324
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                                                                  Local Similarity 46.7%; hes 7; Conservation
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                                      4 KKFKKKLLKSLKRLG 18
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83.3%;
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                                                                                                  Pred. No.
                                                                                                                  Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                Mismatches
                                                                                                  43;
                                                                                                                    DB 10; Length 357;
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Sequence 2, Application US/09952385 Patent No. US20020119504A1 GENERAL INFORMATION: APPLICANT: Andrew, David P.

US-09-952-385-2

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US-09-767-215-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                         Sequence 2, Application US/09767215
Patent No. US20020081636A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
             CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 7; Conserv
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                                                                                    TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-142001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS:
TITLE OF INVENTION: IDENTIFYING MODULATORS OF GPR-9-6 FILE REFERENCE: 1855.1044-003
CURRENT APPLICATION NUMBER: US/10/000,759A
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US/9/522,752
PRIOR FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
PRIOR FILING DATE: 2000-02-09
                                                                                                                                               APPLICANT: Bertin, John
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TYPE: PRT
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TITLE OF INVENTION: ANTI-OPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: LKS98-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/266,464
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CURRENT FILING DATE: 2001-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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46.78;
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Pred. No. 43;
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Pred. No. 43;
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US-09-765-614B-31
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Best Local Similarity
"hehes 9; Conserva
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                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. :
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                      Query Match
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Patent No. US20020081636A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
TITLE OF INVENTION: agents
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                                                                                                                                                                                                                                                                  FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-142001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                      OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:Platelet OTHER INFORMATION: binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                     FEATURE:
                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                              LENGTH: 13
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60.0%;
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60.0%;
47.1%;
75.0%;
                  Score 41;
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Pred. No. 1.3e+02;
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Pred. No. 1.2e+02;
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                  DB 10;
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Best Local Similarity

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TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/09/925,715
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09925715 Patent No. US20020102217A1
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Patent No. US20020151516A1
GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                   NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mixson, James A
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                                                                                                                                                                                APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <Unknown>
                                                                            APPLICATION NUMBER: US/08/985,526
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Wilmington
TELEPHONE: (302) 658-9141
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75.08;
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RESULT 12
US-09-792-793A-91
; Sequence 91, Application U
; Patent No. US20020168370A1
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LENGTH: 70
EARLIER APPLICATION NUMBER: PCT/CA96/00653
EARLIER FILING DATE: 1996-09-26
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 70
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                                                                                                                                                                                                                                                             Sequence 10, Application US/09229304
Patent No. US20020090671A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches 9; Conser
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
                                                                                                             APPLICANT: TAM, Cherk Shing TITLE OF INVENTION: BONE STIMULATING FACTOR FILE REFERENCE: 079997/0123
CURRENT APPLICATION NUMBER: US/09/229,304
CURRENT FILING DATE: 1999-01-13
EARLIER APPLICATION NUMBER: US 09/048,058
EARLIER FILING DATE: 1998-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 25020-601D CURRENT APPLICATION NUMBER: US/09/792,793A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McDonald, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Human Chemokine polypeptide: PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (302) 658-5613 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Clark-Lewis et. al., JOURNAL: J. Leukoc. Biol. VOLUME: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 703-711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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nes 9; Conserv
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Pred. No.
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Pred. No. 2.3;
1; Mismatches 2
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: LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-768-826-60
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-063-8
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: Sequence 8, Application US/09940063

: Patent No. US20020090657A1
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"here 9; Conserva
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    Query Match
Best Local Similarity
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APPLICANT: Murphy, Kristine E.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: NO. US20020090657Alel Antibodies and Ligands for "Bonzo"
TITLE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 1855.1070-000
CURRENT APPLICATION NUMBER: US/09/940,063
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09.4449,437
PRIOR APPLICATION NUMBER: 09.4449,437
PRIOR APPLICATION NUMBER: 09.4449,437
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                  SOFTWARE: F
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PRIOR APPLICATION NUMBER: PCT/US00/22350
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/148,759
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEC ID NOS: 61
SOFTWARF: DECLING SOFTWARF: DECLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Patent No. US20020012966A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shi et al.
TITLE OF INVENTION: 18 human secreted proteins
FILE REFERENCE: PF512P1
CURRENT APPLICATION NUMBER: US/09/768,826
CURRENT FILING DATE: 2001-01-25
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mes 9; Conserv
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PatentIn Ver. 2.0
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DB 10;
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                                 Length 145;
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